SEQUENCE LISTING

<110> Cahoon, Edgar B.
Cahoon, Rebecca E.

<120> Enzymes Involved In Petroselinic Acid Biosynthesis

<130> BB1413 US NA

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<150> 60/169,968
<151> 9 DECEMBER 1999

<160> 12

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<212> DNA
<213> Hedera helix

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<221> unsure
<222> (997)

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<212> PRT
<213> Hedera helix

<220>
<221> UNSURE
<222> (318)

<400> 2

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             20                  25                  30

Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
         35                  40                  45

Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
     50                  55                  60

Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
 65                  70                  75                  80

Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
                 85                  90                  95

Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
            100                 105                 110

Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
        115                 120                 125

Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
    130                 135                 140

Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
145                 150                 155                 160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
                165                 170                 175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
            180                 185                 190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
        195                 200                 205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
    210                 215                 220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
225                 230                 235                 240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
                245                 250                 255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
            260                 265                 270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
        275                 280                 285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
    290                 295                 300
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Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
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Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
385 390

<210> 3
<211> 445
<212> DNA
<213> Hedera helix

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gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240
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ttgtgcggaa acaactggcg ctgccgctga ttctgcaagt cactggagag tcaaaattcg 360
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<212> PRT
<213> Hedera helix

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Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser
20 25 30

Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val
65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95

Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly
100 105 110

Lys Lys
114

<210> 5
<211> 920
<212> DNA
<213> Hedera helix

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catcgatttc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180
gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240
cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
ttgtgcggaa acaactggcg ctgccggctg attctgcagt cactggagag tcaaaattcg 360
cagcgcttgg ggctgattct ctcgacacgg ttgagattgt gatgggacta gaggaggaat 420
tcggaatcag cgtggaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480
acctgattga gaagcttgtt gagaaaaagg agtagaagaa ccggggtaga aattctgcaa 540
aataggttta ttaaggacag ttactttatt aggatggttc atcaagatct tcattaccct 600
acatttattt gtatgctcct catgaagccg caaaagtagt agtggtgatg aaatttaccc 660
cgagtcttcg ccttaattat caaagtgaga gagccagaaa aagaggctat gctatctctc 720
atctcgttat gttttatttt cttgtcggac ttctggttgg agtttttttt ttttatctaa 780
acatgatatt agtcttgttt aaaagtttct caaaaaaata tatcttgttg ttgagactga 840
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<211> 137
<212> PRT
<213> Hedera helix

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1 5 10 15

Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser
20 25 30

Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val
65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95

Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu
100 105 110

Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
115 120 125

Ile Glu Lys Leu Val Glu Lys Lys Glu
130 135

<210> 7
<211> 385
<212> PRT
<213> Coriandrum sativum

<400> 7

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Met Ala Met Lys Leu Asn Ala Leu Met Thr Leu Gln Cys Pro Lys Arg
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Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser
            20                  25                  30

Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp
        35                  40                  45

Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu
    50                  55                  60

Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu
65                  70                  75                  80

Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala
                85                  90                  95

Phe Glu Asp Gln Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro
            100                 105                 110

Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala
        115                 120                 125

Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp
    130                 135                 140

Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp
145                 150                 155                 160

Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr
                165                 170                 175

Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr
            180                 185                 190

Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met
        195                 200                 205

Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
    210                 215                 220

Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala
225                 230                 235                 240

Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala
                245                 250                 255

Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr
            260                 265                 270

Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala
        275                 280                 285
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His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr
    290   295   300

Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp
305   310   315   320

Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly
                325   330   335

Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala
            340   345   350

Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys
        355   360   365

Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile
    370   375   380

Ile
385

<210> 8
<211> 137
<212> PRT
<213> Coriandrum sativum

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Met Ala Ala Phe Thr Ala Ser Ser Val Ser Phe Thr Pro Leu Ser Ile
 1   5   10   15

Ser Leu Asn Gln Thr Lys Gly Phe Ala Arg Gly Ser Val Ser Ile Pro
            20   25   30

Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu
        35   40   45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Glu Thr Val Glu Lys Val
    50   55   60

Cys Glu Ile Val Lys Lys Gln Leu Ala Leu Pro Pro Thr Thr Glu Val
65   70   75   80

Ser Gly Asp Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
                85   90   95

Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu
            100   105   110

Glu Glu Ser Ala Gln Ala Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
        115   120   125

Ile Glu Lys Leu Cys Glu Lys Lys Glu
    130   135

<210> 9
<211> 1381
<212> DNA
<213> Hedera helix

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aagaagaacc accctgctgc gtttgctaag tcaccattac cagtgaccag agttagctct 180
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<211> 394
<212> PRT
<213> Hedera helix

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Phe Ala Lys Ser Pro Leu Pro Val Thr Arg Val Ser Ser Pro Arg Val
20 25 30

Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
35 40 45

Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
50 55 60

Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
65 70 75 80

Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
85 90 95

Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
100 105 110

Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
115 120 125

Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
130 135 140

Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
145 150 155 160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
165 170 175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
180 185 190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
195 200 205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
210 215 220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
225 230 235 240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
245 250 255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
260 265 270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
275 280 285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
290 295 300

Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Gly Val Tyr
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
355 360 365

Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
385 390

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<213> Artificial Sequence

<220>
<223> PCR primer

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<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
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